



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/658,355A
Source: IFW
Date Processed by STIC: 3/16/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221

Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS.

<http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: <u>10/658,355 A</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 <input checked="" type="checkbox"/> Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <input type="checkbox"/> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <input type="checkbox"/> Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 <input type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <input type="checkbox"/> Variable Length	Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <input type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 <input type="checkbox"/> Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 <input type="checkbox"/> Use of <220>	Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 00/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 <input type="checkbox"/> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <input type="checkbox"/> Misuse of n/Xaa	"n" can only represent a single <u>nucleotide</u> ; "Xaa" can only represent a single <u>amino acid</u>	



IFWO

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/658,355A

DATE: 03/16/2004

TIME: 07:58:57

Input Set : D:\923seq.002

Output Set: N:\CRF4\03162004\J658355A.raw

3 <110> APPLICANT: Gantier, Rene
 4 Guyon, Thierry
 5 Hugo, Cruz Ramos
 6 Vega, Manuel
 7 Drittanti, Lila
 9 <120> TITLE OF INVENTION: Rational Directed Protein Evolution Using Two Dimensional
 10 Rational
 11 Mutagenesis Scanning
 13 <130> FILE REFERENCE: 38751-923
 15 <140> CURRENT APPLICATION NUMBER: US/10/658,355A
 16 <141> CURRENT FILING DATE: 2003-09-08
 18 <150> PRIOR APPLICATION NUMBER: 60/457,063
 19 <151> PRIOR FILING DATE: 2003-03-21
 21 <150> PRIOR APPLICATION NUMBER: 60/410,258
 22 <151> PRIOR FILING DATE: 2002-09-09
 24 <160> NUMBER OF SEQ ID NOS: 501
 25 <170> SOFTWARE: FastSEQ for Windows Version 4.0

Does Not Comply
 Check and Update Sequence

(pg. 1-6)

ERRORED SEQUENCES

7445 <210> SEQ ID NO: 182
 7446 <211> LENGTH: 55
 7447 <212> TYPE: DNA
 7448 <213> ORGANISM: Artificial Sequence
 7450 <220> FEATURE:
 7451 <223> OTHER INFORMATION: EcoRI Forward Primer
 7453 <400> SEQUENCE: 182

E--> 7454 gcctgtatga tttattggat gttggaattc cctgatgcgg tattttctcc ttacg

7455 (55)

7457 <210> SEQ ID NO: 183

7458 <211> LENGTH: 55

7459 <212> TYPE: DNA

7460 <213> ORGANISM: Artificial Sequence

7462 <220> FEATURE:

7463 <223> OTHER INFORMATION: EcoRI Reverse Primer

7465 <400> SEQUENCE: 183

E--> 7466 cgttaaggaga aaataccgca tcagggaatt ccaacatcca ataaatcata caggc

7467 (55)

7469 <210> SEQ ID NO: 184

7470 <211> LENGTH: 35

7471 <212> TYPE: DNA

7472 <213> ORGANISM: Artificial Sequence

please see
 item # "1"
 on error
 summary
 sheet.

55
 insert
 here

55
 insert
 here

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/658,355A

DATE: 03/16/2004
TIME: 07:58:58

Input Set : D:\923seq.002
Output Set: N:\CRF4\03162004\J658355A.raw

*SAME
errors*

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7474 <220> FEATURE:
7475 <223> OTHER INFORMATION: Seq ClaI Forward Primer
7477 <400> SEQUENCE: 184
E--> 7478 ctgattatca accgcggtac atatgattga catgc
      (35)
7479
7481 <210> SEQ ID NO: 185
7482 <211> LENGTH: 31
7483 <212> TYPE: DNA
7484 <213> ORGANISM: Artificial Sequence
7486 <220> FEATURE:
7487 <223> OTHER INFORMATION: Seq ClaI Reverse Primer
7489 <400> SEQUENCE: 185
E--> 7490 tacgggataa taccgcgccca catagcagaa c
      (31)
7491
7493 <210> SEQ ID NO: 186
7494 <211> LENGTH: 18
7495 <212> TYPE: DNA
7496 <213> ORGANISM: Artificial Sequence
7498 <220> FEATURE:
7499 <223> OTHER INFORMATION: Seq Forward Primer
7501 <400> SEQUENCE: 186
E--> 7502 cctgatgaag gaggactc
      (18)
7503
7505 <210> SEQ ID NO: 187
7506 <211> LENGTH: 18
7507 <212> TYPE: DNA
7508 <213> ORGANISM: Artificial Sequence
7510 <220> FEATURE:
7511 <223> OTHER INFORMATION: Seq Reverse Primer
7513 <400> SEQUENCE: 187
E--> 7514 ccaagcagca gatgagtc
      (18)
7515
7517 <210> SEQ ID NO: 188
7518 <211> LENGTH: 31
7519 <212> TYPE: DNA
7520 <213> ORGANISM: Artificial Sequence
7522 <220> FEATURE:
7523 <223> OTHER INFORMATION: IFN alpha-2b 5' Primer
7525 <400> SEQUENCE: 188
E--> 7526 tcaagctgcaa gtcaagctgc tctgtgggct g
      (31)
7527
7529 <210> SEQ ID NO: 189
7530 <211> LENGTH: 48
7531 <212> TYPE: DNA
7532 <213> ORGANISM: Artificial Sequence
7534 <220> FEATURE:
7535 <223> OTHER INFORMATION: IFN alpha-2b 3' Primer
7537 <400> SEQUENCE: 189
E--> 7538 gctctagatc attccttact tcttaaaact tcttgcaagt ttgttgac

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/658,355A

DATE: 03/16/2004

TIME: 07:58:58

Input Set : D:\923seq.002

Output Set: N:\CRF4\03162004\J658355A.raw

Same errors

7539 48
 7541 <210> SEQ ID NO: 190
 7542 <211> LENGTH: 36
 7543 <212> TYPE: DNA
 7544 <213> ORGANISM: Artificial Sequence
 7546 <220> FEATURE:
 7547 <223> OTHER INFORMATION: IFN alpha-2b HindIII Primer
 7549 <400> SEQUENCE: 190
 E--> 7550 cccaagctta tggccttgac ctttgcttta ctggtg 36
 7551
 7553 <210> SEQ ID NO: 191
 7554 <211> LENGTH: 48
 7555 <212> TYPE: DNA
 7556 <213> ORGANISM: Artificial Sequence
 7558 <220> FEATURE:
 7559 <223> OTHER INFORMATION: IFN alpha-2b XbaI Primer
 7561 <400> SEQUENCE: 191
 E--> 7562 gctctagatc attccttact tottaaactt tcttgcaagt ttgttgac 48
 7563
 7565 <210> SEQ ID NO: 192
 7566 <211> LENGTH: 80
 7567 <212> TYPE: DNA
 7568 <213> ORGANISM: Artificial Sequence
 7570 <220> FEATURE:
 7571 <223> OTHER INFORMATION: IFN alpha-2b 80 bp 5' Primer
 7573 <400> SEQUENCE: 192
 E--> 7574 cccaagctta tggccttgac ctttgcttta ctggtggccc tcttggtgct cagctgcaag 60
 E--> 7575 80
 E--> 7576 tcaagctgct ctgtgggctg
 7578 <210> SEQ ID NO: 193
 7579 <211> LENGTH: 20
 7580 <212> TYPE: DNA
 7581 <213> ORGANISM: Artificial Sequence
 7583 <220> FEATURE:
 7584 <223> OTHER INFORMATION: EMCV Forward Primer
 7586 <400> SEQUENCE: 193
 E--> 7587 ccgctacatt gaggcattcca
 7588
 7590 <210> SEQ ID NO: 194
 7591 <211> LENGTH: 21
 7592 <212> TYPE: DNA
 7593 <213> ORGANISM: Artificial Sequence
 7595 <220> FEATURE:
 7596 <223> OTHER INFORMATION: EMCV Reverse Primer
 7598 <400> SEQUENCE: 194
 E--> 7599 caggagcagg acaaggtcac t
 7600
 7602 <210> SEQ ID NO: 195
 7603 <211> LENGTH: 22

RAW SEQUENCE LISTING

DATE: 03/16/2004

PATENT APPLICATION: US/10/658,355A

TIME: 07:58:58

Input Set : D:\923seq.002

Output Set: N:\CRF4\03162004\J658355A.raw

*SAME
errors*

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7604 <212> TYPE: DNA
7605 <213> ORGANISM: Artificial Sequence
7607 <220> FEATURE:
7608 <221> NAME/KEY: misc_feature
7609 <222> LOCATION: 1; 22
7610 <223> OTHER INFORMATION: EMCV Probe: n at position 1 is a 5-carboxyfluorescein
7611 (FAM)-modified deoxycytidylate; n at position 22 is an N,N,N',N'-
7612 tetramethyl-6-carboxyrhodamine (TAMRA)-modified deoxythymidylate.
7614 <400> SEQUENCE: 195
E--> 7615 naagcgtca agacccaacc gcg
7616 (22)
8074 <210> SEQ ID NO: 208
8075 <211> LENGTH: 41
8076 <212> TYPE: DNA
8077 <213> ORGANISM: Artificial Sequence
8079 <220> FEATURE:
8080 <223> OTHER INFORMATION: Oligonucleotide
8082 <400> SEQUENCE: 208
E--> 8083 aacatattgtg tgatctgcct caaaccaca gcctgggtag c
8084 (41)
8086 <210> SEQ ID NO: 209
8087 <211> LENGTH: 46
8088 <212> TYPE: DNA
8089 <213> ORGANISM: Artificial Sequence
8091 <220> FEATURE:
8092 <223> OTHER INFORMATION: Oligonucleotide
8094 <400> SEQUENCE: 209
E--> 8095 aaggatcctc attccttact tcttaaactt tcttgcaagt ttgttg
8096 (46)
8098 <210> SEQ ID NO: 210
8099 <211> LENGTH: 41
8100 <212> TYPE: DNA
8101 <213> ORGANISM: Artificial Sequence
8103 <220> FEATURE:
8104 <223> OTHER INFORMATION: Oligonucleotide
8106 <400> SEQUENCE: 210
E--> 8107 aacatattgtg tgatctgcct caaaccaca gcctgggtag c
8108 (41)
8110 <210> SEQ ID NO: 211
8111 <211> LENGTH: 46
8112 <212> TYPE: DNA
8113 <213> ORGANISM: Artificial Sequence
8115 <220> FEATURE:
8116 <223> OTHER INFORMATION: Oligonucleotide
8118 <400> SEQUENCE: 211
E--> 8119 aaggatcctc attccttact tcttaaactt tcttgcaagt ttgttg
8120 (46)
19072 <210> SEQ ID NO: 500
19073 <211> LENGTH: 46

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/658,355A

DATE: 03/16/2004

TIME: 07:58:59

Input Set : D:\923seq.002

Output Set: N:\CRF4\03162004\J658355A.raw

Same errors

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19074 <212> TYPE: DNA
19075 <213> ORGANISM: Artificial Sequence
19077 <220> FEATURE:
19078 <223> OTHER INFORMATION: primer reverse INFA-E159H
19080 <400> SEQUENCE: 500
E--> 19081 aaggatcctc attccttact tottaaactg tgttgcaagt ttgttg
19082 46
19084 <210> SEQ ID NO: 501
19085 <211> LENGTH: 46
19086 <212> TYPE: DNA
19087 <213> ORGANISM: Artificial Sequence
19089 <220> FEATURE:
19090 <223> OTHER INFORMATION: primer reverse INFA-E159Q
19092 <400> SEQUENCE: 501
E--> 19093 aaggatcctc attccttact tottaaactc tgttgcaagt ttgttg
19094 46

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/658,355A

DATE: 03/16/2004

TIME: 07:59:00

Input Set : D:\923seq.002

Output Set: N:\CRF4\03162004\J658355A.raw

L:7454 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:55 SEQ:182
L:7466 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:55 SEQ:183
L:7478 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:35 SEQ:184
L:7490 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:31 SEQ:185
L:7502 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:18 SEQ:186
L:7514 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:18 SEQ:187
L:7526 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:31 SEQ:188
L:7538 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:48 SEQ:189
L:7550 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:36 SEQ:190
L:7562 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:48 SEQ:191
L:7574 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:192
M:254 Repeated in SeqNo=192
L:7587 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:193
L:7599 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:21 SEQ:194
L:7615 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:195 after pos.:0
L:7615 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:22 SEQ:195
L:8083 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:41 SEQ:208
L:8095 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:46 SEQ:209
L:8107 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:41 SEQ:210
L:8119 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:46 SEQ:211
L:19081 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:46 SEQ:500
L:19093 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:46 SEQ:501